

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/733,306C
Source: IFW/b
Date Processed by STIC: 11/19/04

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IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/733,306C

DATE: 11/19/2004

TIME: 10:56:57

Input Set : A:\9022-20 (Substitute).ST25.txt

Output Set: N:\CRF4\11192004\I733306C.raw

3 <110> APPLICANT: Childrens Hospital
 4 Schwarz, Margaret A.
 6 <120> TITLE OF INVENTION: METHODS OF FACILITATING VASCULAR GROWTH IN CARDIAC MUSCLE
 AND
 7 METHODS FOR THE PRODUCTION OF RECOMBINANT EMAP II
 9 <130> FILE REFERENCE: 9022-20
 11 <140> CURRENT APPLICATION NUMBER: US 09/733,306C
 12 <141> CURRENT FILING DATE: 2000-12-08
 14 <150> PRIOR APPLICATION NUMBER: US 60/171,874
 15 <151> PRIOR FILING DATE: 1999-12-23
 17 <150> PRIOR APPLICATION NUMBER: US 60/197,558
 18 <151> PRIOR FILING DATE: 2000-04-17
 20 <150> PRIOR APPLICATION NUMBER: US 60/231,759
 21 <151> PRIOR FILING DATE: 2000-09-12
 23 <150> PRIOR APPLICATION NUMBER: US 60/241,138
 24 <151> PRIOR FILING DATE: 2000-10-17
 26 <160> NUMBER OF SEQ ID NOS: 4
 28 <170> SOFTWARE: PatentIn version 3.2
 30 <210> SEQ ID NO: 1
 31 <211> LENGTH: 14
 32 <212> TYPE: PRT
 33 <213> ORGANISM: Artificial sequence
 35 <220> FEATURE:
 36 <223> OTHER INFORMATION: Synthetic polypeptide
 38 <400> SEQUENCE: 1
 40 Cys Asp Ala Phe Pro Gly Glu Pro Asp Lys Glu Leu Asn Pro
 41 1 5 10
 44 <210> SEQ ID NO: 2
 45 <211> LENGTH: 1086
 46 <212> TYPE: DNA
 47 <213> ORGANISM: Mus musculus
 50 <220> FEATURE:
 51 <221> NAME/KEY: CDS
 52 <222> LOCATION: (64)..(993)
 54 <400> SEQUENCE: 2
 55 gaggtgctc aagagctgcg gttgggtcac cgcttcatgt ttctctgccg attctgggga 60
 57 aag atg gca acg aat gat gct gtt ctg aag agg ctg gag cag aag ggt 108
 58 Met Ala Thr Asn Asp Ala Val Leu Lys Arg Leu Glu Gln Lys Gly
 59 1 5 10 15
 61 gca gag gcg gat cag atc atc gaa tat ctc aag cag cag gtt gct ctt 156
 62 Ala Glu Ala Asp Gln Ile Ile Glu Tyr Leu Lys Gln Gln Val Ala Leu
 63 20 25 30
 65 ctt aag gag aaa gca att ttg cag gca aca atg aga gaa gaa aag aaa 204
 66 Leu Lys Glu Lys Ala Ile Leu Gln Ala Thr Met Arg Glu Glu Lys Lys

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133 atg gcc aat agt gga att aaa taagtgtct gtaactgaaa gacattggcg      1023
134 Met Ala Asn Ser Gly Ile Lys
135      305                      310
137 aaaacttaat aacaataaag agaagtgtgt ttatcactta catataaaaa aaaaaaaaaa      1083
139 aaa
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143 <211> LENGTH: 310
144 <212> TYPE: PRT
145 <213> ORGANISM: Mus musculus
147 <400> SEQUENCE: 3
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153 Glu Ala Asp Gln Ile Ile Glu Tyr Leu Lys Gln Gln Val Ala Leu Leu
154      20                      25                      30
157 Lys Glu Lys Ala Ile Leu Gln Ala Thr Met Arg Glu Glu Lys Lys Leu
158      35                      40                      45
161 Arg Val Glu Asn Ala Lys Leu Lys Lys Glu Ile Glu Glu Leu Lys Gln
162      50                      55                      60
165 Glu Leu Ile Leu Ala Glu Ile His Asn Gly Val Glu Gln Val Arg Val
166 65                      70                      75                      80
169 Arg Leu Ser Thr Pro Leu Gln Thr Asn Cys Thr Ala Ser Glu Ser Val
170      85                      90                      95
173 Val Gln Ser Pro Ser Val Ala Thr Thr Ala Ser Pro Ala Thr Lys Glu
174      100                     105                     110
177 Gln Ile Lys Ala Gly Glu Glu Lys Lys Val Lys Glu Lys Thr Glu Lys
178      115                     120                     125
181 Lys Gly Glu Lys Lys Glu Lys Gln Gln Ser Ala Ala Ala Ser Thr Asp
182      130                     135                     140
185 Ser Lys Pro Ile Asp Ala Ser Arg Leu Asp Leu Arg Ile Gly Cys Ile
186 145                     150                     155                     160
189 Val Thr Ala Lys Lys His Pro Asp Ala Asp Ser Leu Tyr Val Glu Glu
190      165                     170                     175
193 Val Asp Val Gly Glu Ala Ala Pro Arg Thr Val Val Ser Gly Leu Val
194      180                     185                     190
197 Asn His Val Pro Leu Glu Gln Met Gln Asn Arg Met Val Val Leu Leu
198      195                     200                     205
201 Cys Asn Leu Lys Pro Ala Lys Met Arg Gly Val Leu Ser Gln Ala Met
202      210                     215                     220
205 Val Met Cys Ala Ser Ser Pro Glu Lys Val Glu Ile Leu Ala Pro Pro
206 225                     230                     235                     240
209 Asn Gly Ser Val Pro Gly Asp Arg Ile Thr Phe Asp Ala Phe Pro Gly
210      245                     250                     255
213 Glu Pro Asp Lys Glu Leu Asn Pro Lys Lys Lys Ile Trp Glu Gln Ile
214      260                     265                     270
217 Gln Pro Asp Leu His Thr Asn Ala Glu Cys Val Ala Thr Tyr Lys Gly
218      275                     280                     285
221 Ala Pro Phe Glu Val Lys Gly Lys Gly Val Cys Arg Ala Gln Thr Met
222      290                     295                     300
225 Ala Asn Ser Gly Ile Lys

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226 305                               310
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230 <211> LENGTH: 312
231 <212> TYPE: PRT
232 <213> ORGANISM: Homo sapiens
234 <400> SEQUENCE: 4
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240 Glu Ala Asp Gln Ile Ile Glu Tyr Leu Lys Gln Gln Val Ser Leu Leu
241                               20                               25                               30
244 Lys Glu Lys Ala Ile Leu Gln Ala Thr Leu Arg Glu Glu Lys Lys Leu
245                               35                               40                               45
248 Arg Val Glu Asn Ala Lys Leu Lys Lys Glu Ile Glu Glu Leu Lys Gln
249                               50                               55                               60
252 Glu Leu Ile Gln Ala Glu Ile Gln Asn Gly Val Lys Gln Ile Ala Phe
253 65                               70                               75                               80
256 Pro Ser Gly Thr Pro Leu His Ala Asn Ser Met Val Ser Glu Asn Val
257                               85                               90                               95
260 Ile Gln Ser Thr Ala Val Thr Thr Val Ser Ser Gly Thr Lys Glu Gln
261                               100                              105                              110
264 Ile Lys Gly Gly Thr Gly Asp Glu Lys Lys Ala Lys Glu Lys Ile Glu
265                               115                              120                              125
268 Lys Lys Gly Glu Lys Lys Glu Lys Lys Gln Gln Ser Ile Ala Gly Ser
269                               130                              135                              140
272 Ala Asp Ser Lys Pro Ile Asp Val Ser Arg Leu Asp Leu Arg Ile Gly
273 145                              150                              155                              160
276 Cys Ile Ile Thr Ala Arg Lys His Pro Asp Ala Asp Ser Leu Tyr Val
277                               165                              170                              175
280 Glu Glu Val Asp Val Gly Glu Ile Ala Pro Arg Thr Val Val Ser Gly
281                               180                              185                              190
284 Leu Val Asn His Val Pro Leu Glu Gln Met Gln Asn Arg Met Val Ile
285                               195                              200                              205
288 Leu Leu Cys Asn Leu Lys Pro Ala Lys Met Arg Gly Val Leu Ser Gln
289                               210                              215                              220
292 Ala Met Val Met Cys Ala Ser Ser Pro Glu Lys Ile Glu Ile Leu Ala
293 225                              230                              235                              240
296 Pro Pro Asn Gly Ser Val Pro Gly Asp Arg Ile Thr Phe Asp Ala Phe
297                               245                              250                              255
300 Pro Gly Glu Pro Asp Lys Glu Leu Asn Pro Lys Lys Lys Ile Trp Glu
301                               260                              265                              270
304 Gln Ile Gln Pro Asp Leu His Thr Asn Asp Glu Cys Val Ala Thr Tyr
305                               275                              280                              285
308 Lys Gly Val Pro Phe Glu Val Lys Gly Lys Gly Val Cys Arg Ala Gln
309                               290                              295                              300
312 Thr Met Ser Asn Ser Gly Ile Lys
313 305                               310

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/733,306C

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